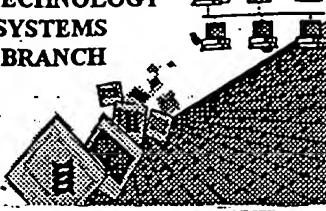# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/004, 219_

Source: _, 01PE_

Date Processed by STIC: _6-10-02_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
                   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

OIPE

RAW SEQUENCE LISTING   DATE: 06/10/2002
PATENT APPLICATION: US/10/004,219   TIME: 15:42:24

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\06102002\J004219.raw

```
 3 <110> APPLICANT: Macrozyme
 4        Aerts, Johannes M.F.G.
 5        Boot, Rolf G.
 7 <120> TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
 8        its use in therapy or prophylaxis against diseases in
 9        which mucus is involved or infection diseases
11 <130> FILE REFERENCE: 2183-5136US
13 <140> CURRENT APPLICATION NUMBER: 10/004,219
14 <141> CURRENT FILING DATE: 2002-06-03
16 <160> NUMBER OF SEQ ID NOS: 14
18 <170> SOFTWARE: PatentIn Ver. 2.1
```

C-->

ERRORED SEQUENCES

```
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 476
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence: human AMCase
26        amino acid sequence deduced from cDNA sequence
28 <400> SEQUENCE: 1
29 Met Thr Lys Leu Ile Leu Leu Thr Gly Leu Val Leu Ile Leu Asn Leu
30 1               5                   10                  15
32 Gln Leu Gly Ser Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala
33             20                  25                  30
35 Gln Tyr Arg Pro Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro
36         35                  40                  45
38 Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn
39     50                  55                  60
41 Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe
42 65                  70                  75                  80
44 Asn Gly Leu Lys Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile
45             85                  90                  95
47 Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr
48             100                 105                 110
50 Pro Glu Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg
51         115                 120                 125
53 Gln Tyr Glu Phe Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser
54     130                 135                 140
56 Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln
57 145                 150                 155                 160
```

W-->
E-->

```
 59 Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro
 60              165                 170                 175
 62 Arg Leu Met Val Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln
 63              180                 185                 190
 65 Ser Gly Tyr Glu Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His
 66              195                 200                 205
 68 Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu
 69     210                 215                 220
 71 Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr
 72 225                 230                 235                 240
 74 Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro
 75              245                 250                 255
 77 Ala Glu Lys Leu Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile
 78              260                 265                 270
 80 Leu Ser Asn Pro Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala
 81              275                 280                 285
 83 Gly Pro Ala Gly Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr
 84     290                 295                 300
 86 Glu Ile Cys Thr Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala
 87 305                 310                 315                 320
 89 Pro Gln Glu Val Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr
 90              325                 330                 335
 92 Asp Asn Ile Lys Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn
 93              340                 345                 350
 95 Lys Phe Gly Gly Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr
 96              355                 360                 365
 98 Gly Thr Phe Cys Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys
 99     370                 375                 380
101 Lys Ala Leu Gly Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro
102 385                 390                 395                 400
104 Ile Glu Pro Ile Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly
105              405                 410                 415
107 Ser Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val
108              420                 425                 430
110 Arg Ala Asn Gly Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp
111              435                 440                 445
113 His Cys Val Asn Gly Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu
114     450                 455                 460
116 Val Phe Asp Thr Ser Cys Asp Cys Cys Asn Trp Ala
117 465                 470                 475
412 <210> SEQ ID NO: 4
413 <211> LENGTH: 473
414 <212> TYPE: PRT
415 <213> ORGANISM: Artificial Sequence
416 <220> FEATURE:
416 <223> OTHER INFORMATION: Description of Artificial Sequence: mouse AMCase
417      amino acid sequence deduced from cDNA sequence
419 <400> SEQUENCE: 4
420 Met Ala Lys Leu Leu Leu Val Thr Gly Leu Ala Leu Leu Leu Asn Ala
```

W--> (annotation pointing to line 416 <220> FEATURE:)

E--> (annotation pointing to line 419 <400> SEQUENCE: 4)

See page 1 (handwritten annotation)

```
421   1                    5                   10                  15
423 Gln Leu Gly Ser Ala Tyr Asn Leu Ile Cys Tyr Phe Thr Asn Trp Ala
424             20                  25                  30
426 Gln Tyr Arg Pro Gly Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro
427         35                  40                  45
429 Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn
430     50                  55                  60
432 Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe
433 65                  70                  75                  80
435 Asn Asp Leu Lys Asn Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile
436              85                  90                  95
438 Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr
439             100                 105                 110
441 Ser Gln Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg
442         115                 120                 125
444 Gln Tyr Gly Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser
445     130                 135                 140
447 Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Lys
448 145                 150                 155                 160
450 Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro
451             165                 170                 175
453 Arg Leu Met Val Thr Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln
454             180                 185                 190
456 Ala Gly Tyr Glu Ile Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His
457         195                 200                 205
459 Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu
460     210                 215                 220
462 Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr
463 225                 230                 235                 240
465 Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro
466             245                 250                 255
468 Ala Glu Lys Leu Ile Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile
469             260                 265                 270
471 Leu Arg Asn Pro Ser Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp
472         275                 280                 285
474 Gly Pro Ala Gly Ala Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr
475     290                 295                 300
477 Glu Ile Cys Thr Phe Leu Arg Ser Gly Ala Thr Glu Val Trp Asp Ala
478 305                 310                 315                 320
480 Ser Gln Glu Val Pro Tyr Ala Tyr Lys Ala Asn Glu Trp Leu Gly Tyr
481             325                 330                 335
483 Asp Asn Ile Lys Ser Phe Ser Val Lys Ala Gln Trp Leu Lys Gln Asn
484         340                 345                 350
486 Asn Phe Gly Gly Ala Met Ile Trp Ala Ile Asp Leu Asp Asp Phe Thr
487     355                 360                 365
489 Gly Ser Phe Cys Asp Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn
490     370                 375                 380
492 Lys Ala Leu Gly Ile Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro
493 385                 390                 395                 400
```

RAW SEQUENCE LISTING   DATE: 06/10/2002
PATENT APPLICATION: US/10/004,219   TIME: 15:42:24

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\06102002\J004219.raw

```
495 Ser Glu Pro Val Thr Thr Pro Pro Gly Ser Gly Ser Gly Gly Gly Ser
496             405             410             415
498 Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp
499             420             425             430
501 Gly Leu Tyr Pro Val Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile
502         435             440             445
504 Asn Gly Ile Thr Tyr Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp
505     450             455             460
507 Thr Ser Cys Asn Cys Cys Asn Trp Pro ..
508 465             470
```

VERIFICATION SUMMARY   DATE: 06/10/2002
PATENT APPLICATION: US/10/004,219   TIME: 15:42:25

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF3\06102002\J004219.raw**

```
L:14  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:28  M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:1
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:416 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:419 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:4
```